SEQUENCE LISTING

<110> DIDEBERG, OTTO
VERNET, THIERRY
MOUZ, NICOLAS

<120> STREPTOCOCCUS PNEUMONIAE PBP2X MINI-PROTEIN AND USES THEREOF

<130> 70457-19

<140> 10/520,655
<141> 2005-03-07

<150> PCT/IB03/003397
<151> 2003-07-11

<150> FR 02/08724
<151> 2002-07-11

<160> 18

<170> PatentIn Ver. 3.3

<210> 1
<211> 551
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic mini-PBP2x construct

<400> 1

```
Gly Ser Gly Ala Lys Arg Gly Thr Ile Tyr Asp Arg Asn Gly Val Pro
  1               5                  10                  15

Ile Ala Glu Asp Ala Thr Ser Gly Gly Pro Asn Arg Ser Tyr Pro Asn
             20                  25                  30

Gly Gln Phe Ala Ser Ser Phe Ile Gly Gly Gly Met Glu Ser Ser Leu
         35                  40                  45

Asn Ser Ile Leu Ala Gly Gly Gly Gly Asp Gly Lys Asp Val Tyr Thr
     50                  55                  60

Thr Ile Ser Ser Pro Leu Gln Ser Phe Met Glu Thr Gln Met Asp Ala
 65                  70                  75                  80

Phe Gln Glu Lys Val Lys Gly Lys Tyr Met Thr Ala Thr Leu Val Ser
                 85                  90                  95

Ala Lys Thr Gly Glu Ile Leu Ala Thr Thr Gln Arg Pro Thr Phe Asp
            100                 105                 110

Ala Asp Thr Lys Glu Gly Ile Thr Glu Asp Phe Val Trp Arg Asp Ile
        115                 120                 125

Leu Tyr Gln Ser Asn Tyr Glu Pro Gly Ser Thr Met Lys Val Met Met
    130                 135                 140

Leu Ala Ala Ala Ile Asp Asn Asn Thr Phe Pro Gly Gly Glu Val Phe
145                 150                 155                 160
```

```
Asn Ser Ser Glu Leu Lys Ile Ala Asp Ala Thr Ile Arg Asp Trp Asp
                165                 170                 175

Val Asn Glu Gly Leu Thr Gly Gly Arg Met Met Thr Phe Ser Gln Gly
            180                 185                 190

Phe Ala His Ser Ser Asn Val Gly Met Thr Leu Leu Glu Gln Lys Met
        195                 200                 205

Gly Asp Ala Thr Trp Leu Asp Tyr Leu Asn Arg Phe Lys Phe Gly Val
    210                 215                 220

Pro Thr Arg Phe Gly Leu Thr Asp Glu Tyr Ala Gly Gln Leu Pro Ala
225                 230                 235                 240

Asp Asn Ile Val Asn Ile Ala Gln Ser Ser Phe Gly Gln Gly Ile Ser
                245                 250                 255

Val Thr Gln Thr Gln Met Ile Arg Ala Phe Thr Ala Ile Ala Asn Asp
            260                 265                 270

Gly Val Met Leu Glu Pro Lys Phe Ile Ser Ala Ile Tyr Asp Pro Asn
        275                 280                 285

Asp Gln Thr Ala Arg Lys Ser Gln Lys Glu Ile Val Gly Asn Pro Val
    290                 295                 300

Ser Lys Asp Ala Ala Ser Leu Thr Arg Thr Asn Met Val Leu Val Gly
305                 310                 315                 320

Thr Asp Pro Val Tyr Gly Thr Met Tyr Asn His Ser Thr Gly Lys Pro
                325                 330                 335

Thr Val Thr Val Pro Gly Gln Asn Val Ala Leu Lys Ser Gly Thr Ala
            340                 345                 350

Gln Ile Ala Asp Glu Lys Asn Gly Gly Tyr Leu Val Gly Leu Thr Asp
        355                 360                 365

Tyr Ile Phe Ser Ala Val Ser Met Ser Pro Ala Glu Asn Pro Asp Phe
    370                 375                 380

Ile Leu Tyr Val Thr Val Gln Gln Pro Glu His Tyr Ser Gly Ile Gln
385                 390                 395                 400

Leu Gly Glu Phe Ala Asn Pro Ile Leu Glu Arg Ala Ser Ala Met Lys
                405                 410                 415

Asp Ser Leu Asn Leu Gln Thr Thr Ala Lys Ala Leu Glu Gln Val Ser
            420                 425                 430

Gln Gln Ser Pro Tyr Pro Met Pro Ser Val Lys Asp Ile Ser Pro Gly
        435                 440                 445

Asp Leu Ala Glu Glu Leu Arg Arg Asn Leu Val Gln Pro Ile Val Val
    450                 455                 460

Gly Thr Gly Thr Lys Ile Lys Asn Ser Ser Ala Glu Glu Gly Lys Asn
465                 470                 475                 480

Leu Ala Pro Asn Gln Gln Val Leu Ile Leu Ser Asp Lys Ala Glu Glu
                485                 490                 495
```

Val Pro Asp Met Tyr Gly Trp Thr Lys Glu Thr Ala Glu Thr Leu Ala
500 505 510

Lys Trp Leu Asn Ile Glu Leu Glu Phe Gln Gly Ser Gly Ser Thr Val
515 520 525

Gln Lys Gln Asp Val Arg Ala Asn Thr Ala Ile Lys Asp Ile Lys Lys
530 535 540

Ile Thr Leu Thr Leu Gly Asp
545 550

<210> 2
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 2
gtcgacttag tctcctaaag ttaatttaat ttttttaatg tttttg 46

<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 3
ggatccggga caggcactcg c 21

<210> 4
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 4
cataaatagt cccacgtttg gccccggatc cacgcggaac cag 43

<210> 5
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 5

gtttgggtaa ctacgattgg gacctccaga ggttgcatcc tcagcaatcg g 51

<210> 6
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 6
gttcaaggaa ctctccattc caccgccgat aaaactagaa gcaaattg 48

<210> 7
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 7
tgtataaaca tccttaccgt ccccacctcc ccctgcaaga atactgttc 49

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 8
ccgcatatgg ccaaacgtgg gactatttat 30

<210> 9
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 9
ggctcgagtt agtctcctaa agttaatgta at 32

<210> 10
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (3)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (4)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (5)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (6)
<223> Asp or Ser

<220>
<221> MOD_RES
<222> (10)..(12)
<223> variable amino acid

<400> 10
Arg Gly Xaa Xaa Xaa Xaa Arg Ser Gly Xaa Xaa Xaa Ala
1 5 10

<210> 11
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (2)..(3)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (5)
<223> variable amino acid

<400> 11
Xaa Xaa Xaa Pro Xaa Gly
1 5

<210> 12
<211> 10
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)
<223> Gly or Tyr

<220>
<221> MOD_RES
<222> (2)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (4)..(6)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (8)..(9)
<223> variable amino acid

<400> 12
Xaa Xaa Glu Xaa Xaa Xaa Asp Xaa Xaa Leu
1 5 10

<210> 13
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (2)..(3)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (4)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (5)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (7)..(9)

<223> variable amino acid

<400> 13
Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Gln
1 5 10

<210> 14
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (2)
<223> Gly or Ser

<220>
<221> MOD_RES
<222> (4)..(5)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (6)..(9)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (12)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (13)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (14)
<223> Asp or Asn

<400> 14
Thr Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Ser Pro Xaa Xaa Xaa
1 5 10

<210> 15
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)

<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (4)
<223> Ala or Gly

<220>
<221> MOD_RES
<222> (6)..(7)
<223> variable amino acid

<400> 15
Xaa Glu Pro Xaa Ser Xaa Xaa Lys
1 5

<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (2)..(3)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (5)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (7)
<223> hydrophobic amino acid

<400> 16
Xaa Xaa Xaa Ser Xaa Asn Xaa
1 5

<210> 17
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 17
Ala Lys Arg Gly Thr Ile Tyr
1 5

<210> 18
<211> 750
<212> PRT
<213> Streptococcus pneumoniae

<400> 18
Met Lys Trp Thr Lys Arg Val Ile Arg Tyr Ala Thr Lys Asn Arg Lys
1 5 10 15

Ser Pro Ala Glu Asn Arg Arg Arg Val Gly Lys Ser Leu Ser Leu Leu
20 25 30

Ser Val Phe Val Phe Ala Ile Phe Leu Val Asn Phe Ala Val Ile Ile
35 40 45

Gly Thr Gly Thr Arg Phe Gly Thr Asp Leu Ala Lys Glu Ala Lys Lys
50 55 60

Val His Gln Thr Thr Arg Thr Val Pro Ala Lys Arg Gly Thr Ile Tyr
65 70 75 80

Asp Arg Asn Gly Val Pro Ile Ala Glu Asp Ala Thr Ser Tyr Asn Val
85 90 95

Tyr Ala Val Ile Asp Glu Asn Tyr Lys Ser Ala Thr Gly Lys Ile Leu
100 105 110

Tyr Val Glu Lys Thr Gln Phe Asn Lys Val Ala Glu Val Phe His Lys
115 120 125

Tyr Leu Asp Met Glu Glu Ser Tyr Val Arg Glu Gln Leu Ser Gln Pro
130 135 140

Asn Leu Lys Gln Val Ser Phe Gly Ala Lys Gly Asn Gly Ile Thr Tyr
145 150 155 160

Ala Asn Met Met Ser Ile Lys Lys Glu Leu Glu Ala Ala Glu Val Lys
165 170 175

Gly Ile Asp Phe Thr Thr Ser Pro Asn Arg Ser Tyr Pro Asn Gly Gln
180 185 190

Phe Ala Ser Ser Phe Ile Gly Leu Ala Gln Leu His Glu Asn Glu Asp
195 200 205

Gly Ser Lys Ser Leu Leu Gly Thr Ser Gly Met Glu Ser Ser Leu Asn
210 215 220

Ser Ile Leu Ala Gly Thr Asp Gly Ile Ile Thr Tyr Glu Lys Asp Arg
225 230 235 240

Leu Gly Asn Ile Val Pro Gly Thr Glu Gln Val Ser Gln Arg Thr Met
245 250 255

Asp Gly Lys Asp Val Tyr Thr Thr Ile Ser Ser Pro Leu Gln Ser Phe
260 265 270

Met Glu Thr Gln Met Asp Ala Phe Gln Glu Lys Val Lys Gly Lys Tyr
275 280 285

Met Thr Ala Thr Leu Val Ser Ala Lys Thr Gly Glu Ile Leu Ala Thr

```
290                 295                 300

Thr Gln Arg Pro Thr Phe Asp Ala Asp Thr Lys Glu Gly Ile Thr Glu
305                 310                 315                 320

Asp Phe Val Trp Arg Asp Ile Leu Tyr Gln Ser Asn Tyr Glu Pro Gly
                325                 330                 335

Ser Thr Met Lys Val Met Met Leu Ala Ala Ala Ile Asp Asn Asn Thr
            340                 345                 350

Phe Pro Gly Gly Glu Val Phe Asn Ser Ser Glu Leu Lys Ile Ala Asp
        355                 360                 365

Ala Thr Ile Arg Asp Trp Asp Val Asn Glu Gly Leu Thr Gly Gly Arg
    370                 375                 380

Met Met Thr Phe Ser Gln Gly Phe Ala His Ser Ser Asn Val Gly Met
385                 390                 395                 400

Thr Leu Leu Glu Gln Lys Met Gly Asp Ala Thr Trp Leu Asp Tyr Leu
                405                 410                 415

Asn Arg Phe Lys Phe Gly Val Pro Thr Arg Phe Gly Leu Thr Asp Glu
            420                 425                 430

Tyr Ala Gly Gln Leu Pro Ala Asp Asn Ile Val Asn Ile Ala Gln Ser
        435                 440                 445

Ser Phe Gly Gln Gly Ile Ser Val Thr Gln Thr Gln Met Ile Arg Ala
    450                 455                 460

Phe Thr Ala Ile Ala Asn Asp Gly Val Met Leu Glu Pro Lys Phe Ile
465                 470                 475                 480

Ser Ala Ile Tyr Asp Pro Asn Asp Gln Thr Ala Arg Lys Ser Gln Lys
                485                 490                 495

Glu Ile Val Gly Asn Pro Val Ser Lys Asp Ala Ala Ser Leu Thr Arg
            500                 505                 510

Thr Asn Met Val Leu Val Gly Thr Asp Pro Val Tyr Gly Thr Met Tyr
        515                 520                 525

Asn His Ser Thr Gly Lys Pro Thr Val Thr Val Pro Gly Gln Asn Val
    530                 535                 540

Ala Leu Lys Ser Gly Thr Ala Gln Ile Ala Asp Glu Lys Asn Gly Gly
545                 550                 555                 560

Tyr Leu Val Gly Leu Thr Asp Tyr Ile Phe Ser Ala Val Ser Met Ser
                565                 570                 575

Pro Ala Glu Asn Pro Asp Phe Ile Leu Tyr Val Thr Val Gln Gln Pro
            580                 585                 590

Glu His Tyr Ser Gly Ile Gln Leu Gly Glu Phe Ala Asn Pro Ile Leu
        595                 600                 605

Glu Arg Ala Ser Ala Met Lys Asp Ser Leu Asn Leu Gln Thr Thr Ala
    610                 615                 620

Lys Ala Leu Glu Gln Val Ser Gln Gln Ser Pro Tyr Pro Met Pro Ser
```

625 630 635 640

Val Lys Asp Ile Ser Pro Gly Asp Leu Ala Glu Glu Leu Arg Arg Asn
645 650 655

Leu Val Gln Pro Ile Val Val Gly Thr Gly Thr Lys Ile Lys Asn Ser
660 665 670

Ser Ala Glu Glu Gly Lys Asn Leu Ala Pro Asn Gln Gln Val Leu Ile
675 680 685

Leu Ser Asp Lys Ala Glu Glu Val Pro Asp Met Tyr Gly Trp Thr Lys
690 695 700

Glu Thr Ala Glu Thr Leu Ala Lys Trp Leu Asn Ile Glu Leu Glu Phe
705 710 715 720

Gln Gly Ser Gly Ser Thr Val Gln Lys Gln Asp Val Arg Ala Asn Thr
725 730 735

Ala Ile Lys Asp Ile Lys Lys Ile Thr Leu Thr Leu Gly Asp
740 745 750